IN THE SPECIFICATION:

Please amend the specification as shown:

Please delete paragraph [019] on page 6, and replace it with the following paragraph:

[019] **FIG. 1.** Comparison of deduced *D. melanogaster* cDNA SD07655 **(SEQ ID NO: 1)** and human MRP1 **(SEQ ID NO: 6)** amino acid sequences. The two amino acid sequences were aligned using ClustalW. Identical residues are marked with shading. The transmembrane regions are noted by a fine underline and the ATP-binding domains are noted by a bold underline. The amino acids derived from exons 4 and 8 of the dMRP gene are presented in bold characters. The small vertical lines above and below the amino acids denote the exon junctions with the type of splice junction marked by a number noting the class: 0, 1 or 2. The dMRP amino acid sequence differs from that of sequence AY069827 at the following positions : L/V pos. 124, M/L pos. 318 and I/T pos. 448.

Please delete paragraph [022] on pages 7-8, and replace it with the following paragraph:

[022] **FIG. 4.** Amino acid alignment of dMRP variable exon 4 (A) **(SEQ ID NOS 7 & 8)** and 8 (B) **(SEQ ID NOS 9-15)** encoded peptides with the cognate peptides from other organisms. The variant dMRP peptide sequence and the equivalent sequences

from *Drosophila* sulfonylurea receptor (Dsur, NG_000795) **(SEQ ID NOS 134 & 138)** and three human MRPs (MRP1, NM_004996 **(SEQ ID NOS 131 & 135)**; MRP2, NP_005836 **(SEQ ID NOS 132 & 136)**; and MRP3, Y17151 **(SEQ ID NOS 133 & 137)**) were aligned using ClustalW. Pfam **(SEQ ID NO: 139)** refers to pfam00664, a consensus sequence for ABC transporter Membrane Spanning Domains. Gaps were introduced to maximize sequence identity and are shown by a horizontal dash. Residues that are identical in at least half of the sequences have their background shaded and those present in more than half of the sequences are listed in the consensus (Cons). (C) Dendrogram constructed with the data of part (B) of the Figure (see *infra* for details).

Please delete paragraph [024] on page 8, and replace it with the following paragraph:

[024] **Fig. 6.** Comparison of deduced *A. gambiae* gMRP1a-d **(SEQ ID NOS 2-5)**, *Drosophila melanogaster* dMRP **(SEQ ID NO: 1)**, and human MRP1 **(SEQ ID NO: 6)** amino acid sequences. The alignment was produced using ClustalW. Identical residues in at least half of the sequences are marked with shading. The different topological regions are indicated in bold and italic above the sequences, and are delimitated by vertical bars. *MSD1-3*, Membrane Spanning Domains 1 to 3; L_0, cytoplasmic loop; *NBD1-2,* Nucleotide Binding Domain, *Linker*, region linking the two halves of the protein. Walker A and Walker B are indicated as *A* and *B*, and their sequences are

marked in bold, as well as the signature (*C*) of ABC transporters. The vertical lines in bold inside the amino acid sequences denote the exon junctions. Where several genes shared the same site, this one was emphasized by a delimitating box.

Please delete paragraph [052] on pages 21-22, and replace it with the following paragraph:

[052] DNA (10 µg) was digested with either *Bam*HI or *Hind*III and the fragments were separated by electrophoresis on a 0.8% agarose gel. Following transfer to Hybond-N nylon membrane and fixation, hybridization was carried out at 65°C (in 1% BSA, 0.25 M NaH_2PO_4 pH 7.2, 1 mM EDTA, 150 µg/ml salmon sperm DNA) with a PCR-derived *dMRP* probe covering 378 bases (forward primer: GATCCGTTTATTTCCTTGCCGC **(SEQ ID NO: 53)**; reverse primer: TCCAGGGCAGTGATTACCAGT **(SEQ ID NO: 54)**). After hybridization, the blot was washed (in 40 mM NaH_2PO_4 pH 7.2, 1% SDS, and 1 mM EDTA) 1X at RT and 2X at 65 C°.

Please delete Table 3, on page 31, and replace it with the Table at Tab A.

Please delete Table 5, on page 39, and replace it with the Table at Tab B.

TABLE 3. Intron-exon organization of the *Drosophila* dMRP gene

Exon					Intron		
n°	Size (bp)	3' acceptor[a] **(SEQ ID NOS 55-72, respectively, in order of appearance)**	exon location[b]	5' donor **(SEQ ID NOS 73-90, respectively, in order of appearance)**	n°	Phase	Size (bp)
1	181		-127•54	TTCTGG / gtgagt	1	0	74
2	1512	gaacag / AACGCA	129•1640	ATTAAG /gtgagt	2	0	135
3	138	acatag / GTGCTC	1776•1913	TTCCTG / gtaaga	3	0	128
4a	147	acaaag / GTTTCC	2042•2188	GCCGAG / gtacag	4	0	146
4b	147	ttttag / GTTTCA	2335•2481	GTGCAA / gtaagt	5	0	800
5	85	gaatag / ACGCAA	3282•3366	CTAAAC / gtaaga	6	1	62
6	820	atacag / CCCATC	3429•4248	TTCCAT / gtaagt	7	2	67
7	371	ttttag / CTCCGT	4316•4686	GCCAAG / gtaagt	8	1	904
8a	221	ttctag / TCGCGA	5591•5811	TATATG / gtaatt	9	0	336
8b	221	tcgaag / TTGTTA	6148•6368	TTTGCG / gtaatt	10	0	385
8c	221	ttccag / TTACCT	6754•6974	TTTGCG / gtaaat	11	0	525
8d	221	atgcag / TGCTAT	7500•7720	TTCGGG / gtaaag	12	0	691
8e	224	tcccag / GTGTGC	8412•8635	TTTATG / gtattt	13	0	4965
8f	221	agctag / GTCTTT	13605•13825	TTTCAG / gtaatc	14	0	1141
8g	221	tcgcag / GTTTCA	14967•15187	TTCGAG / gtaatt	15	0	340
9	218	ggttag / GTTCTG	15528•15745	AGATCG / gtatgt	16	2	64
10	507	cttcag / CTTTAT	15810•16316	GTTCAG / gtaagc	17	2	59
11	382	atttag / AATAAT	16376•16757	ATTCAG / gtgggt	18	0	4791
12	393	ctatag / AAAACC	21549•21941				

Table 5. Organization of exon-intron junctions in the *gMRPs*

	Exon					Intron		
Name		Location on protein sequence[a]	Size (bp)	3' acceptor[b] **(SEQ ID NOS 91-110, respectively, in order of appearance)**	5' donor[b] **(SEQ ID NOS 111-130, respectively, in order of appearance)**	Name	Phase	Size (bp)
MRP1a	1		165		CCCTTG/gtgaga	1	0	83
	2	10	234	gtacag/GTGGAC	TCCTTG/gtaagc	2	0	202
	3	88	566	cttcag/GTGGGC	GCTGAG/gtaagt	3	2	224
	4	277	3638	atatag/ATTACT				
MRP1b	1		ND[c]		TTTTGG/gtaagt	1	0	603
	2	13	300	ttacag/GACGAT	GCTTAT/gtaagt	2	0	76
	3	113	2144	tttcag/ATTATG	ATACCA/gtaagt	3	2	63
	4	804	1458	ctctag/GGAACT	CTTCAG/gtatgt	4	2	73
	5	1315	382	ttccag/AATTGT	ATTCAG/gtaaga	5	0	65
	6	1441	493	acacag/AAAACA				
MRP1c	1		418		GCTTAT/gtgagt	1	0	69
	2	113	662	atttag/ATCGAC	GATGCA/gtaagt	2	2	96
	3	334	1497	ttatag/AGAACT	TTATCA/gtaagt	3	2	61
	4	833	77	ttttag/GGAACT	ATGAAG/gtaagt	4	1	60
	5	858	1369	tttcag/AAATAT	CTTCAG/gttagt	5	2	63
	6	1315	382	atctag/AATTGT	ATTCAG/gtgaga	6	0	71
	7	1442	293	ttacag/AAAACA				
MRP1d	1		ND[c]		GCTTAT/gtgagt	1	0	69
	2	113	662	atttag/ATCGAC	CATGCA/gtacgt	2	2	110
	3	334	1497	tcgcag/AGAAAT	ATACCA/gtgagt	3	2	65
	4	833	80	tttcag/ACAACT	AAGACG/gtaggt	4	1	98
	5	859	1372	caccag/AAATTA	CTTCAG/gtatct	5	2	73
	6	1317	382	ttccag/AATTGT	ATTCAG/gtaaga	6	0	65
	7	1444	363	ccacag/AAAACA				

a) The numbering is based on amino acid one being the putative first Met.
b) Capital letters are used for the sequence in the exon and small case letters for sequence in the intron.
c) Not Determined.